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A. Nelson

#12

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P/S

RAW SEQUENCE LISTING DATE: 06/05/2000
 PATENT APPLICATION: US/09/142,108A TIME: 11:41:24

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\06022000\I142108A.raw

4 <110> APPLICANT: International Flower Developments Pty Ltd
 6 <120> TITLE OF INVENTION: Genetic sequences encoding flavonoid pathway enzymes
 7 and uses therefor
 9 <130> FILE REFERENCE: 2088133
 11 <140> CURRENT APPLICATION NUMBER: 09/142108A
 C--> 12 <141> CURRENT FILING DATE: 1999-03-29
 14 <150> PRIOR APPLICATION NUMBER: PN8386
 15 <151> PRIOR FILING DATE: 1996-03-01
 17 <160> NUMBER OF SEQ ID NOS: 41
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1789
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Petunia x hybrida
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (50)..(1588)
 30 <400> SEQUENCE: 1
 31 gcaggattt gtgaacccca tagaagtaaa atactcctat ctttatttc atg gaa atc 58
 32 Met Glu Ile
 33 1
 35 tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106
 36 Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
 37 5 10 15
 39 att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tta cca cca 154
 40 Ile Leu Arg Ser Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
 41 20 25 30 35
 43 ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202
 44 Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
 45 40 45 50
 47 aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
 48 Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu
 49 55 60 65
 51 atg tat ctt aag atg ggg ttc gta gac gtc gtt gca gcc tcg gca 298
 52 Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
 53 70 75 80
 55 tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346
 56 Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
 57 85 90 95
 59 cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat 394
 60 Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp
 61 100 105 110 115
 63 ctt gtt ttt gca cct tat gga cct aga tgg cgt atg ctt agg aaa att 442
 64 Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile
 65 120 125 130
 67 tgc tca gtt cac ctt ttc tct acc aag gct tta gat gac ttc cgc cat 490
 68 Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His

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69	135	140	145	
71	gtc cgc cag gat gaa gtg aaa aca ctg acg cgc gca cta gca agt gca			538
72	Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala			
73	150	155	160	
75	ggc caa aag cca gtc aaa tta ggt cag tta ttg aac gtg tgc acg acg			586
76	Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr			
77	165	170	175	
79	aac gca ctc gcg cga gta atg cta ggt aag cga gta ttt gcc gac gga			634
80	Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly			
81	180	185	190	195
83	agt ggc gat gtt gat cca caa gcg gcg gag ttc aag tca atg gtg gtg			682
84	Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val			
85	200	205	210	
87	gaa atg atg gta gtc gcc ggt gtt ttt aac att ggt gat ttt att ccg			730
88	Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp Phe Ile Pro			
89	215	220	225	
91	caa ctt aat tgg tta gat att caa ggt gta gcc gct aaa atg aag aag			778
92	Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys Lys			
93	230	235	240	
95	ctc cac gcg cgt ttc gac gcg ttc ttg act gat ata ctt gaa gag cat			826
96	Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu His			
97	245	250	255	
99	aag ggt aaa att ttt gga gaa atg aaa gat ttg ttg agt act ttg atc			874
100	Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu Ile			
101	260	265	270	275
103	tct ctt aaa aat gat gat gcg gat aat gat gga ggg aaa ctc act gat			922
104	Ser Leu Lys Asn Asp Ala Asp Asn Asp Gly Gly Lys Leu Thr Asp			
105	280	285	290	
107	aca gaa att aaa gca tta ctt ttg aac ttg ttt gta gct gga aca gac			970
108	Thr Glu Ile Lys Ala Leu Leu Asn Leu Phe Val Ala Gly Thr Asp			
109	295	300	305	
111	aca tct tct aat gca gtt gaa tgg gcc att gct gag ctt att cgt aat			1018
112	Thr Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn			
113	310	315	320	
115	cca aaa ata cta gcc caa gcc cag caa gag atc gac aaa gtc gtt gga			1066
116	Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val Gly			
117	325	330	335	
119	agg gac cgg cta gtt ggc gaa ttg gac cta gcc caa ttg aca tac ttg			1114
120	Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr Leu			
121	340	345	350	355
123	gaa gct ata gtc aag gaa acc ttt cgg ctt cat cca tca acc cct ctt			1162
124	Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu			
125	360	365	370	
127	tca ctt cct aca att gca tct gag agt tgt gag atc aat ggc tat ttg			1210
128	Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr Phe			
129	375	380	385	
131	att cca aaa ggc tca acg ctt ctc ctt aat gtt tgg gcc att gct cgt			1258
132	Ile Pro Lys Gly Ser Thr Leu Leu Asn Val Trp Ala Ile Ala Arg			
133	390	395	400	

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135 gat cca aat gca tgg gct gat cca ttg gag ttt agg cct gaa agg ttt 1306
 136 Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe
 137 405 410 415
 139 ttg cca gga ggt gag aag ccc aaa gtt gat gtc cgt ggg aat gac ttt 1354
 140 Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp Phe
 141 420 425 430 435
 143 gaa gtc ata cca ttt gga gct gga cgt agg att tgt gct gga atg aat 1402
 144 Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Asn
 145 440 445 450
 147 ttg ggt ata cgt atg gtc cag ttg atg att gca act tta ata cat gca 1450
 148 Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His Ala
 149 455 460 465
 151 ttt aac tgg gat ttg gtc agt gga caa ttg ccg gag atg ttg aat atg 1498
 152 Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn Met
 153 470 475 480
 155 gaa gaa gca tat ggg ctg acc tta caa ccg gct gat cca ttg gtt gtg 1546
 156 Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val
 157 485 490 495
 159 cac cca agg cct cgc tta gaa gcc caa gcg tac att ggg tga 1588
 160 His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
 161 500 505 510
 163 gcagcaacag cccatggaga taacatgagt gttaaatgta tgagtctcca tatctgttt 1648
 165 agtttgat tgctttggat tttagtagttt ttatattgtt agatcaatgt ttgcattgtc 1708
 167 agtaagataa tccgttgctt gttcattaa ctccaggtgg acaataaaag aagtaatttg 1768
 169 tatgaaaaaaaaaaaaaaa a 1789
 172 <210> SEQ ID NO: 2
 173 <211> LENGTH: 512
 174 <212> TYPE: PRT
 175 <213> ORGANISM: Petunia x hybrida
 177 <400> SEQUENCE: 2
 178 Met Glu Ile Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu
 179 1 5 10 15
 180 Leu Gln Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro
 181 20 25 30
 182 Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His
 183 35 40 45
 184 Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr
 185 50 55 60
 186 Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Ala
 187 65 70 75 80
 188 Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn
 189 85 90 95
 190 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn
 191 100 105 110
 192 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu
 193 115 120 125
 194 Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp
 195 130 135 140
 196 Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/142,108A

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TIME: 11:41:25

Input Set : A:\PTO.txt
Output Set: N:\CRF3\06022000\I142108A.raw

197 145 150 155 160
198 Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val
199 165 170 175
200 Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
201 180 185 190
202 Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser
203 195 200 205
204 Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
205 210 215 220
206 Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
207 225 230 235 240
208 Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu
209 245 250 255
210 Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
211 260 265 270
212 Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
213 275 280 285
214 Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Phe Val Ala
215 290 295 300
216 Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu
217 305 310 315 320
218 Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Glu Ile Asp Lys
219 325 330 335
220 Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu
221 340 345 350
222 Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser
223 355 360 365
224 Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn
225 370 375 380
226 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala
227 385 390 395 400
228 Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro
229 405 410 415
230 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly
231 420 425 430
232 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala
233 435 440 445
234 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu
235 450 455 460
236 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met
237 465 470 475 480
238 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro
239 485 490 495
240 Leu Val Val His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
241 500 505 510
245 <210> SEQ ID NO: 3
246 <211> LENGTH: 1745
247 <212> TYPE: DNA
248 <213> ORGANISM: Dianthus caryophyllus

VERIFICATION SUMMARY DATE: 06/05/2000
 PATENT APPLICATION: US/09/142,108A TIME: 11:41:26

Input Set : A:\PTO.txt
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:955 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:959 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:963 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:967 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:971 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:975 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:979 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:983 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:987 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:991 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:995 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:999 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1003 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1007 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1011 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1019 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1023 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1027 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1031 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1035 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:1054 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 9, CDS LOCATION:3421..3907
 L:1055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:2833 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
 L:2838 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
 L:2843 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
 L:2848 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
 L:2853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
 L:2878 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2883 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2888 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
 L:2905 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2910 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2915 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2920 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2926 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2941 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
 L:2957 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
 L:2957 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36

VERIFICATION SUMMARY DATE: 06/05/2000
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Input Set : A:\PTO.txt
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L:2957 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:2969 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2974 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2979 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2984 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2989 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2994 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2999 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:3004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3048 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3053 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3058 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3063 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3068 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3073 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3078 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41



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